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GCTCTCCCTGCTCCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTG
M R A L E G P G L S L L
TGCCTGGTGTGGCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAA
C L V L A L P A L L P V P A V R G V A E
ACACCCACCTACCCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGC
T P T Y P W R D A E T G E R L V C A Q C
CCCCAGGCACCTTTGTGCAGCGGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCG
P P G T F V Q R P C R R D S P T T C G P
TGTCCACCGCGCCACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAAC
C P P R H Y T Q F W N Y L E R C R Y C N
GTCCTCTGCGGGGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCC
V L C G E R E E E A R A C H A T H N R A
TGCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGT
C R C R T G F F A H A G F C L E H A S C
CCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCG
P P G A G V I A P G T P S Q N T Q C Q P
TGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGC
C P P G T F S A S S S S S E Q C Q P H R
AACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTG
N C T A L G L A L N V P G S S S H D T L
TGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
C T S C T G F P L S T R V P G A E E C E
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTG
R A V I D F V A F Q D I S I K R L Q R L
CTGCAGGCCCTCGAGGCCCGGAGGGCTGGGCTCCGACACCAAGGGCGGGCGCGCGGCC
L Q A L E A P E G W G P T P R A G R A A
TTGCAGCTGAAGCTGCGTCGGCGGCTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTG
L Q L K L R R R L T E L L G A Q D G A L
CTGGTGCGGCTGCTGCAGGCGCTGCGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTC
L V R L L Q A L R V A R M P G L E R S V
CGTGAGCGCTTCTCCCTGTGCACTGATCCTGGCCCCCTTATTTATTCTACATCCTTG
R E R F L P V H *
GCACCCCACTTGCACTGAAAGAGGCTTTTTTTTAAATAGAAGAAATGAGGTTTCTTAAAG
CTTATTTTTATAAAGCTTTTTTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG.1

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TGGCATGTGGTCAGGCACAGCAGGGTCTGTGTCCGCGCTGAGCCGCGCTCTCCCTGCT
CCAGCAAGGACCATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTG
M R A L E G P G L S L L C L V L
GCGCTGCCTGCCCTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTAC
A L P A L L P V P A V R G V A E T P T Y
CCCTGGCGGGACGCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACC
P W R D A E T G E R L V C A Q C P P G T
TTTGTGCAGCGCCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGC
F V Q R P C R R D S P T T C G P C P P R
CACTACACGCAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGG
H Y T Q F W N Y L E R C R Y C N V L C G
GAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGC
E R E E E A R A C H A T H N R A C R C R
ACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCACGCATCGTGTCCACCTGGTGCC
T G F F A H A G F C L E H A S C P P G A
GGCGTGATTGCCCCGGGTGAGAGCTGGGCGAGGGGAGGGGCCCCAGGAGTGGTGGCCGG
G V I A P G E S W A R G G A P R S G G R
AGGTGTGGCAGGGGTGAGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACACCACTT
R C G R G Q V A G P S L A P *
CCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCAGAACACGCAGTGCCA
GCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCA
CCGCAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACAC
CCTGTGCACCAGCTGCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGC
CTGAGGGGGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGCCCCCTGCACG
TGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGGAAGGGGCCACAGTGGATTTGAGGGG
TCAGGGGTCCCTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGAGAATTT
GGATCTGAGCCAGGGCACAGCCTCCCCTGGAGAGCTCTGGGAAAGTGGGCAGCAATCTCC

FIG.2A

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TAAC TGCC GAGGGAAGGTGGCTGGCTCCTCTGACACGGGGAACCGAGGCCTGATGGT
AACTCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATGGGGAACCGAGGC
CCAATGTTAACCCTGTTGAGAAGTCACAGGGGAAGTGACCCCTTAACATCAAGTCAG
GTCCGGTCCATCTGCAGGTCCCAACTCGCCCCTTCGATGGCCAGGAGCCCCAAGCCCT
TGCCTGGGCCCCCTTGCTCTTGACGCCAAGGTCCGAGTGGCCGCTCCTGCCCCCTAGGC
CTTTGCTCCAGCTCTCTGACCGAAGGCTCCTGCCCCCTTCTCCAGTCCCCATCGTTGCACT
GCCCTCTCCAGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCCGAGTGG
GGCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAGTGTGTGTGGGTGAAATGATCGGAC
CGCTGCCTCCCCACCCCACTGCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTG
TGGCTTTCCAGGACATCTCCATCAAGAGGAGCGGCTGCTGCAGGCC

FIG.2B

1	M	-	G	L	S	T	V	P	D	L	L	P	L	V	L	E	L	V	G	I	Y	P	S	G	V	I	G	L	V	P	H	L	G	D	R	E	-	TNFR1		
1	M	A	P	V	A	V	W	A	A	L	A	V	G	L	E	L	W	A	A	H	A	L	P	A	Q	V	A	-	-	-	-	-	F	T	P	-	-	TNFR2		
1	M	G	A	G	A	T	G	R	A	M	D	-	-	-	G	P	R	L	L	L	L	L	L	G	V	S	L	G	G	A	K	E	-	A	C	P	-	-	NGFR	
1	M	-	R	L	P	R	-	A	S	S	P	C	G	L	A	W	G	P	L	L	L	G	L	V	A	S	Q	P	Q	L	V	P	P	-	-	-	-	LT6R		
1	M	L	G	T	W	T	-	-	-	L	P	L	V	L	T	S	V	-	A	R	L	S	S	K	S	V	N	A	Q	V	T	D	I	N	S	K	G	L	FAS	
1	M	-	-	-	-	-	A	R	P	H	P	-	-	-	W	W	L	C	V	L	G	T	L	V	G	L	S	-	A	T	P	A	P	K	S	C	P	-	CD27	
1	M	R	V	L	-	-	-	-	-	-	-	-	-	-	-	L	A	A	L	G	L	L	F	L	G	A	L	R	A	-	-	-	F	P	Q	-	-	CD30		
1	M	V	R	L	P	L	-	Q	-	-	-	C	V	L	-	W	G	C	L	L	-	-	-	-	T	A	V	H	P	E	-	-	P	P	-	-	CD40			
1	M	G	N	-	-	-	-	-	-	S	C	Y	N	I	V	A	T	L	L	L	V	L	N	-	-	-	-	-	-	-	-	F	E	R	-	-	4-1BB			
1	M	C	V	G	A	-	-	R	R	L	G	-	-	-	R	G	P	C	A	A	L	L	L	G	L	G	L	S	T	V	T	G	L	H	C	V	-	-	OX40	
1	M	K	S	V	-	L	Y	L	I	-	-	-	L	F	L	S	C	I	I	I	N	G	R	D	A	P	-	-	-	-	-	Y	T	P	-	-	VC22			
1	M	K	S	-	-	-	Y	I	L	L	-	-	L	L	L	S	C	I	I	I	I	N	S	D	I	T	P	-	-	-	-	-	H	E	P	-	-	CRMB		
1	M	R	A	L	E	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	-	V	P	A	-	-	TNFR-6a	
1	M	R	A	L	E	-	-	-	-	-	-	G	P	G	L	S	L	L	C	L	V	L	A	L	P	A	L	L	P	-	-	-	-	-	V	P	A	-	-	TNFR-6b

FIG.3A

39	-	K	R	D	S	V	C	P	Q	G	K	Y	I	H	-	-	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	TNFR1	
32	-	Y	-	A	P	E	P	G	S	T	C	R	L	R	E	Y	Y	D	Q	T	A	Q	M	C	C	S	K	C	S	P	G	Q	H	A	K	V	F	C	-	TNFR2	
34	-	T	-	-	-	-	-	-	-	-	-	-	-	-	G	L	Y	T	H	S	G	E	-	C	C	K	A	C	N	L	G	E	G	V	A	Q	P	C	G	A	NGFR
36	-	Y	R	I	E	N	Q	T	C	W	D	Q	D	K	E	Y	Y	E	P	M	H	D	V	C	C	S	R	C	P	P	G	E	F	V	F	A	V	C	-	Lt6R	
36	E	L	R	K	T	V	T	T	V	E	T	Q	N	L	E	G	L	H	H	D	G	Q	F	C	H	K	P	C	P	P	G	E	R	K	A	R	D	C	T	V	FAS
29	-	E	-	-	-	-	-	-	-	-	-	-	-	-	R	H	Y	W	A	Q	G	K	L	C	Q	M	C	E	P	G	T	F	L	V	K	D	C	D	Q	CD27	
22	-	D	R	P	F	E	D	T	C	H	G	N	P	S	H	Y	Y	D	K	A	V	R	R	C	C	Y	R	C	P	M	G	L	F	P	T	Q	Q	C	P	Q	CD30
24	-	-	-	-	-	T	A	C	R	E	-	-	-	K	Q	Y	L	-	-	I	N	S	Q	-	C	S	L	C	Q	P	G	Q	K	L	V	S	D	C	-	CD40	
21	-	T	R	S	L	Q	D	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	S	N	C	P	A	G	T	F	-	-	-	-	C	D	N	4-1BB	
33	-	G	-	-	-	-	-	-	-	-	-	-	-	-	D	T	Y	P	S	N	D	R	-	C	C	H	E	C	R	P	G	N	G	M	V	S	R	C	S	R	OX40
28	-	P	N	G	K	C	K	D	T	E	Y	K	R	H	N	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	VC22	
26	-	S	N	G	K	C	K	D	N	E	Y	K	R	H	H	-	-	-	-	-	-	L	C	C	L	S	C	P	P	G	T	Y	A	S	R	L	C	D	S	CRMB	
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6a
27	-	V	R	G	V	A	E	T	P	T	Y	P	W	R	D	A	-	E	T	G	E	R	L	V	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	-	-	TNFR-6b

FIG.3B

75	P	-	G	Q	D	T	D	C	R	-	E	C	E	S	G	S	-	F	T	A	S	E	N	H	L	R	H	C	L	S	C	S	K	-	C	R	K	E	M	G	TNFR1
68	T	K	T	S	D	T	V	C	-	D	S	C	-	E	D	S	T	Y	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R	-	C	S	D	Q	V	TNFR2
60	N	Q	-	T	-	V	-	C	E	-	P	C	L	D	S	V	T	F	S	D	V	V	S	A	T	E	P	C	K	P	C	T	-	E	C	V	G	L	Q	S	NGFR
73	S	R	S	Q	D	T	V	C	-	K	T	C	-	P	H	N	S	Y	N	E	H	W	N	H	L	S	T	C	Q	L	C	R	P	-	C	D	I	V	L	G	LTbR
76	H	-	G	D	E	P	D	C	V	-	P	C	Q	E	G	K	E	Y	T	D	K	A	H	F	S	S	K	C	R	R	C	R	L	-	C	D	E	G	H	G	FAS
56	H	R	K	A	-	A	Q	C	D	-	P	C	I	P	G	V	S	F	S	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD27
61	R	-	-	-	P	T	D	C	R	K	Q	C	-	E	P	D	Y	Y	L	D	E	A	D	R	C	T	A	C	V	T	C	S	-	-	-	R	D	D	D	CD30	
52	T	E	F	T	E	T	E	C	-	L	P	C	-	G	E	S	E	F	L	D	T	W	N	R	E	T	H	C	H	Q	H	C	Y	-	C	D	P	N	L	G	CD40
40	N	R	N	Q	-	-	I	C	-	S	P	C	-	P	P	N	S	F	S	S	A	-	G	G	Q	R	T	C	D	I	C	R	-	Q	-	-	-	-	K	G	4-1BB
59	S	Q	N	T	-	V	-	C	R	-	P	C	-	G	P	G	F	Y	N	D	V	V	S	S	K	-	P	C	K	P	C	T	-	W	C	-	N	L	R	S	OX40
60	K	T	N	T	-	-	Q	C	-	T	P	C	-	G	S	G	T	F	T	G	R	N	N	H	L	P	A	C	L	S	C	N	G	R	C	N	S	N	Q	V	VC22
58	K	T	N	T	N	T	Q	C	-	T	P	C	-	A	S	D	T	F	T	S	R	N	N	H	L	P	A	C	L	S	C	N	G	R	C	D	S	N	Q	V	CRMB
63	R	R	D	S	P	T	T	C	-	G	P	C	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	TNFR-6a
63	R	R	D	S	P	T	T	C	-	G	P	C	-	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L	C	G	E	R	E	E	TNFR-6b

FIG.3C

111	-	Q	V	E	I	S	C	T	V	D	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S	L	-	TNFR1	
106	-	-	-	E	T	Q	A	-	C	T	R	E	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	-	G	C	R	L	C	A	P	L	TNFR2
95	M	S	A	P	-	-	-	-	C	V	E	A	D	D	A	V	C	R	C	A	Y	G	Y	-	Q	D	E	T	T	G	-	R	C	E	A	C	R	V	-	NGFR	
110	F	E	E	V	A	P	-	C	T	S	D	R	K	A	E	C	R	C	Q	P	G	M	S	C	V	Y	L	D	N	E	-	-	C	V	H	C	E	E	LTbR		
113	L	E	V	E	I	N	-	C	T	R	T	Q	N	T	K	-	-	-	P	N	-	-	-	-	-	-	-	-	-	-	-	-	-	F	F	C	N	-	-	FAS	
74	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	H	H	T	R	P	-	-	H	C	E	S	C	R	H	-	CD27		
92	L	V	E	K	T	P	-	C	A	W	N	S	S	R	V	C	E	C	R	P	G	M	F	C	S	T	S	A	V	N	-	-	S	C	A	R	C	F	H	CD30	
89	L	R	V	Q	Q	K	-	G	T	S	E	T	D	T	I	C	T	C	E	E	G	W	H	C	T	-	-	S	E	A	-	-	-	C	E	S	C	V	L	H	CD40
71	V	F	R	T	R	K	E	C	S	S	T	S	H	A	E	C	D	C	T	P	G	F	H	C	L	-	-	G	A	-	-	G	C	S	M	C	E	Q	D	4-1BB	
92	G	S	E	R	K	Q	L	C	T	A	T	Q	D	T	V	C	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40	
96	-	-	E	T	R	S	-	C	N	T	T	H	H	R	I	C	E	C	S	P	G	Y	Y	C	L	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	VC22	
96	-	-	E	T	R	S	-	C	N	T	T	H	N	R	I	C	D	C	A	P	G	Y	Y	C	F	L	K	G	S	-	-	G	C	K	A	C	V	S	Q	CRMB	
101	-	-	E	A	R	A	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6a
101	-	-	E	A	R	A	-	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	-	-	-	-	A	H	A	-	-	G	-	-	F	C	L	E	H	TNFR-6b

FIG.3D

149	-	-	-	-	C	L	N	G	T	V	H	L	-	-	S	C	Q	E	K	Q	N	T	V	C	T	-	C	H	A	G	F	F	L	R	E	-	-	-	N	TNFR1		
141	R	-	-	-	C	R	P	G	F	G	V	A	R	P	G	T	E	T	S	D	V	V	-	C	K	P	C	A	P	G	T	F	S	N	T	S	T	D	TNFR2			
128	-	-	-	-	C	E	A	G	S	G	L	V	-	F	S	C	Q	D	K	Q	N	T	V	-	C	E	C	P	D	G	T	Y	S	D	E	A	N	H	V	D	NGFR	
146	R	L	V	L	C	Q	P	G	T	E	A	E	V	T	D	E	I	M	D	T	D	V	N	V	-	C	V	P	C	K	P	G	H	F	Q	N	T	S	P	R	A	LTbR
137	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	T	V	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	FAS		
87	-	-	-	-	C	H	S	G	L	-	L	V	-	R	N	C	T	I	T	A	N	A	E	-	C	A	-	C	R	N	G	W	-	-	-	-	-	-	-	CD27		
129	S	V	-	-	C	P	A	G	M	I	V	K	F	P	G	T	A	Q	K	N	T	V	-	C	E	P	A	S	P	G	V	-	S	P	A	C	A	S	P	E	CD30	
123	R	-	-	S	C	S	P	G	F	G	V	K	Q	I	A	T	G	V	S	D	T	I	-	C	E	P	C	P	V	G	F	F	S	N	V	S	S	A	F	E	CD40	
106	-	-	-	-	C	K	Q	G	Q	E	L	T	K	K	G	-	-	-	-	-	-	-	-	-	C	K	D	C	C	F	G	T	F	N	D	Q	K	R	G	I	-	4-1BB
110	-	-	-	-	-	R	A	G	T	Q	P	L	-	D	S	Y	-	-	K	P	G	V	D	-	C	A	P	C	P	P	G	H	F	S	P	G	D	N	Q	-	OX40	
131	T	-	-	K	C	G	I	G	Y	G	V	S	G	H	-	T	S	V	G	D	V	I	-	C	S	P	C	G	F	G	T	Y	S	H	T	V	S	S	A	D	VC22	
131	T	-	-	K	C	G	I	G	Y	G	V	S	G	H	-	T	P	T	G	D	V	V	-	C	S	P	C	G	L	G	T	Y	S	H	T	V	S	S	V	D	CRMB	
130	A	-	-	S	C	P	P	G	A	G	V	I	A	P	G	T	P	S	Q	N	T	Q	-	C	Q	P	C	P	P	G	T	F	S	A	S	S	S	S	E	TNFR-6a		
130	A	-	-	S	C	P	P	G	A	G	V	I	A	P	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b		

FIG.3E

[illegible]

FIG. 3F

[illegible]

FIG. 3G

[illegible]

FIG. 3H

235	- - - R Y Q R W - K S K L Y S I - - - V C G K S T P E K E G E L E G T T INFR1
280	N C V - - I M T Q V K K K P L C - - - - - TNFR2
269	- - - - Y I A F K R W N S C K Q - - - - - NGFR
250	L C R - - K L G T L L K R H - - - - - LTbR
189	- - - - - W V K R K E V Q K - - - T C R K H R K E N Q G S H E - - - FAS
166	- - - - - F R Q - - - - - CD27
282	E C R P G M I C A T S A T N S C A R C V P Y P I C A A E T V T K P Q D M A E K D CD30
218	- - - - - V A K K - - - - - CD40
193	- - - - - - - - - - - 4-1BB
195	- - - - - W P - - - R - - - OX40
246	- - - Y Q N I S K - - V C T - - - VC22
246	- - - Y Q N I S K - - V C T - - - CRMB
217	D F V - - A F Q D I S I K R - - - - - TNFR-6a
143	- - - - - - - - - - - TNFR-6b

FIG. 31

264	T	K	P	L	A	P	N	P	S	F	S	P	T	P	G	F	T	P	T	L	G	F	S	P	V	P	S	S	T	F	T	S	S	S	T	Y	T	P	G	D	TNFR1
294	-	-	-	-	-	-	L	Q	R	E	A	K	V	P	H	L	P	A	-	D	K	A	R	G	T	Q	G	P	E	Q	Q	H	L	L	I	T	A	-	-	TNFR2	
281	-	-	-	-	-	-	-	-	N	K	Q	G	A	N	S	R	P	P	V	-	N	Q	T	P	P	P	E	G	E	K	L	H	S	D	S	G	I	S	V	D	NGFR
262	-	-	-	-	-	-	-	-	P	E	G	E	S	P	P	C	P	A	-	P	R	A	D	P	H	F	F	D	L	A	E	P	L	-	-	-	-	-	-	LIbR	
212	-	-	-	-	-	-	S	P	T	L	N	P	E	-	-	-	T	V	A	I	N	L	S	D	V	D	L	S	K	Y	I	T	-	-	-	-	-	-	-	FAS	
169	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	P	CD27		
322	T	T	F	E	A	P	P	L	G	T	Q	P	D	C	N	P	T	P	E	-	N	G	E	A	P	A	S	T	S	P	T	Q	S	L	L	V	D	S	Q	A	CD30
222	-	-	-	-	-	-	-	-	P	T	N	K	A	P	H	P	K	Q	E	-	P	Q	-	E	I	N	F	P	D	-	-	-	-	-	-	-	-	-	-	CD40	
193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB		
198	-	-	-	-	-	-	-	-	-	T	S	Q	G	P	S	T	R	P	V	-	E	-	-	-	V	P	G	G	R	A	V	A	A	I	L	G	L	G	L	-	OX40
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	G	S	-	-	S	F	K	Q	-	-	-	L	T	K	-	VC22	
255	-	-	-	-	-	-	-	-	L	N	F	E	I	K	C	N	N	-	-	-	-	-	-	K	D	S	Y	S	S	S	K	Q	-	-	-	L	T	K	-	CRMB	
229	-	-	-	-	-	-	-	-	L	Q	R	L	L	Q	A	L	E	A	P	E	-	G	W	-	-	G	P	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6a
143	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	-	S	W	A	R	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b

FIG.3J

[illegible]

FIG. 3G

[illegible]

FIG. 3K

329	-	-	-	-	L	A	S	D	P	I	P	N	P	L	Q	K	W	E	D	S	A	H	K	P	Q	S	L	D	T	D	D	P	A	T	L	Y	A	V	V	E	TNFR1	
339	-	-	-	-	-	-	-	-	-	D	R	R	A	P	T	R	N	Q	P	Q	A	P	G	V	E	A	S	G	A	G	E	A	R	A	S	T	G	S	S	S	TNFR2	
347	V	E	K	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	G	S	NGFR			
303	-	-	-	-	-	-	-	-	-	A	P	S	L	E	E	V	V	L	Q	Q	S	P	L	-	-	-	-	-	-	-	V	Q	A	R	E	L	-	-	E	A	E	LTbR
240	-	-	-	-	M	T	L	S	Q	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	FAS				
207	G	A	L	F	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H	Q	-	CD27			
401	S	S	A	F	L	L	C	H	R	R	A	C	R	K	R	I	R	Q	K	L	H	L	C	Y	P	V	Q	T	S	Q	P	K	L	E	L	V	D	S	R	P	CD30	
252	-	-	-	-	-	-	-	-	Q	E	T	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD40			
216	G	R	K	K	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB				
245	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40				
281	-	-	-	-	-	-	-	-	-	-	-	-	-	M	S	H	S	E	T	V	T	L	A	G	D	C	L	S	S	V	D	I	Y	I	L	Y	S	N	T	N	VC22	
284	-	-	-	-	-	-	-	-	-	-	-	-	-	M	P	H	S	E	S	V	T	L	V	G	D	C	L	S	S	V	D	I	Y	I	L	Y	S	N	T	N	CRMB	
258	-	-	-	-	-	-	-	-	R	R	R	L	T	E	L	L	G	A	Q	D	G	A	L	L	V	R	L	L	Q	A	L	R	-	-	-	-	-	-	-	-	TNFR-6a	
155	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b				

FIG.3L

365	N	V	P	P	L	R	W	K	E	F	V	R	R	L	G	L	S	D	H	E	I	D	R	L	E	L	Q	N	G	R	C	L	R	E	A	Q	Y	S	M	L	TNFR1	
372	P	G	G	H	G	T	Q	V	N	V	T	C	I	V	N	V	C	S	S	D	H	-	S	S	Q	C	S	Q	A	S	S	T	M	G	D	T	-	-	TNFR2			
355	A	G	D	T	W	R	H	L	A	G	E	L	G	Y	Q	P	E	H	I	D	S	F	T	H	E	A	C	P	V	R	-	-	-	-	-	-	A	L	L	NGFR		
327	P	G	E	H	G	Q	V	A	H	G	A	N	G	I	H	V	T	G	S	V	T	V	T	G	N	I	Y	I	Y	N	G	P	V	L	G	G	T	-	-	LTbR		
246	-	-	-	-	-	-	-	-	K	G	F	V	R	K	N	G	V	N	E	A	K	I	D	E	I	K	N	D	N	V	Q	D	T	A	E	Q	K	V	Q	L	L	FAS
214	-	-	-	-	-	-	-	-	R	R	K	Y	R	S	N	K	G	E	S	P	V	E	P	A	E	P	C	R	Y	S	C	P	R	-	-	-	-	-	-	CD27		
441	R	R	S	S	T	Q	L	R	S	G	A	S	V	T	E	P	V	A	E	E	R	G	L	M	S	Q	P	L	M	E	T	C	H	S	V	G	A	Y	L	CD30		
256	-	-	-	-	-	-	-	-	H	G	C	Q	P	V	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CD40			
222	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4-1BB				
245	-	-	-	-	-	-	-	-	R	L	P	P	D	-	A	H	K	P	P	G	G	S	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OX40			
308	A	Q	D	Y	E	T	D	T	I	S	Y	R	V	G	N	V	L	D	D	D	S	H	M	P	G	S	C	N	I	H	K	-	-	-	-	-	-	-	VC22			
311	T	Q	D	Y	E	T	D	T	I	S	Y	H	V	G	N	V	L	D	V	D	S	H	M	P	G	R	C	D	T	H	K	-	-	-	-	-	-	-	CRMB			
282	-	-	-	-	-	-	-	-	-	-	-	V	A	R	M	P	G	L	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6a			
155	-	-	-	-	-	-	-	-	-	-	-	-	G	R	R	C	G	R	G	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TNFR-6b				

FIG.3M

[illegible]

FIG. 3N

[illegible]

FIG. 30

449	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	P A P S L L R	TNFR1
448	P - - - -	- - - - -	L P L G V P D A G M K P S	- - - - -	- - - - -	- - - - -	TNFR2
413	L V E S L C S E S	- - - - -	- - - - -	- - - - -	- - - - -	T A T S P V	NGFR
403	H - - - -	- - - - -	L A E T - E T L G C Q D L	- - - - -	- - - - -	- - - - -	LTbR
329	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	N E I Q S L V FAS	FAS
247	I Q E D - Y R K P	- - - - -	- - - - -	- - - - -	- - - - -	E P A C S P CD27	CD27
560	Y P E Q E T E P P L G S C S D V M L S V E E E G K E D P L P T A A S G K CD30	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CD30
270	R - - - -	- - - - -	I S V Q - E R Q	- - - - -	- - - - -	- - - - -	CD40
236	Q E E D G C - - - - S C - - - - R F P E E E E G - - - - - G C E L 4-1BB	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	4-1BB
263	I Q E E Q A D A H - - - - -	- - - - -	- - - - -	- - - - -	- - - - -	S T L A K I OX40	OX40
349	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	VC22
355	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	CRMB
296	F - - - -	- - - - -	L P V - - - - - H	- - - - -	- - - - -	- - - - -	TNFR-6α
168	L - - - -	- - - - -	A P	- - - - -	- - - - -	- - - - -	TNFR-6β

FIG. 3P

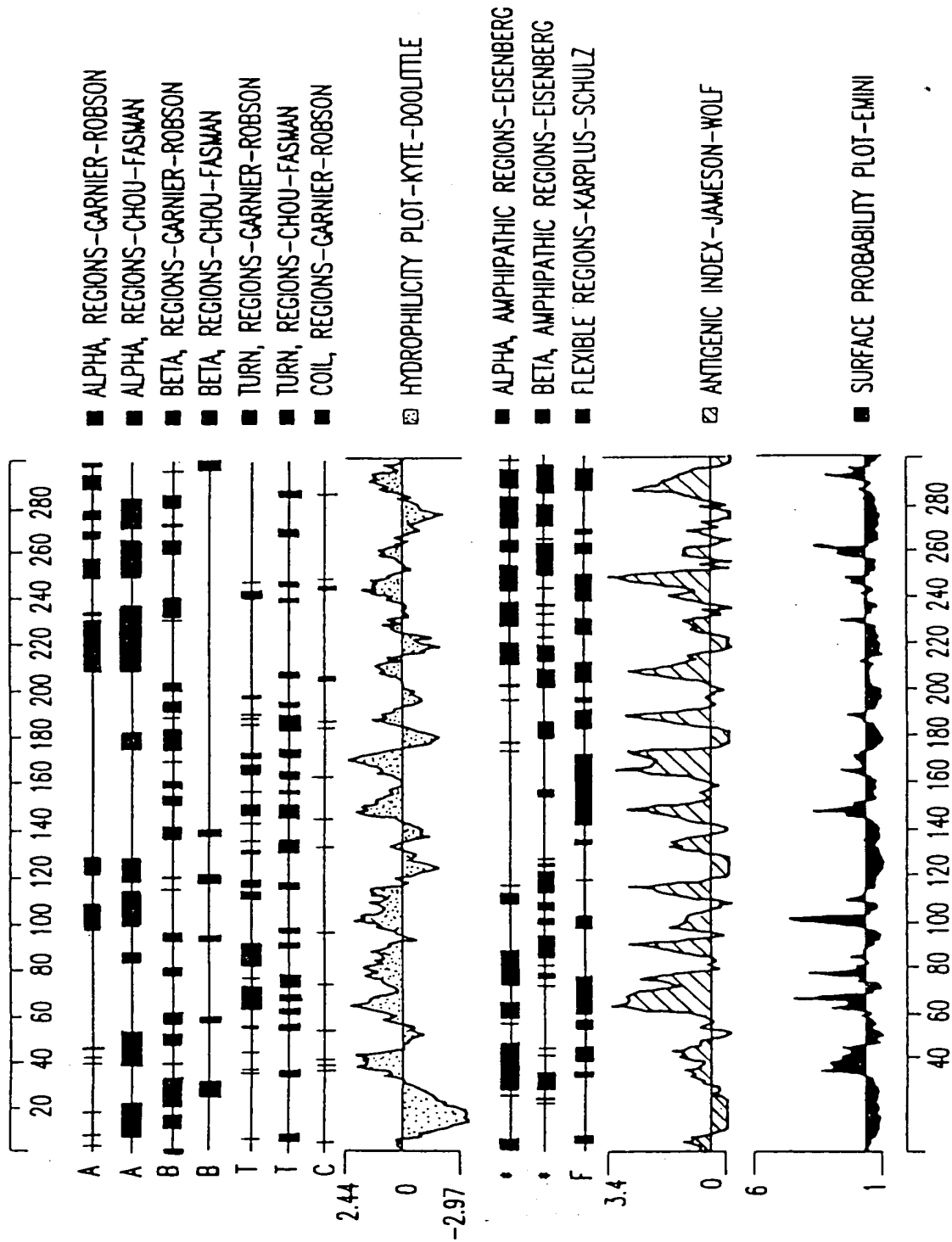


FIG.4

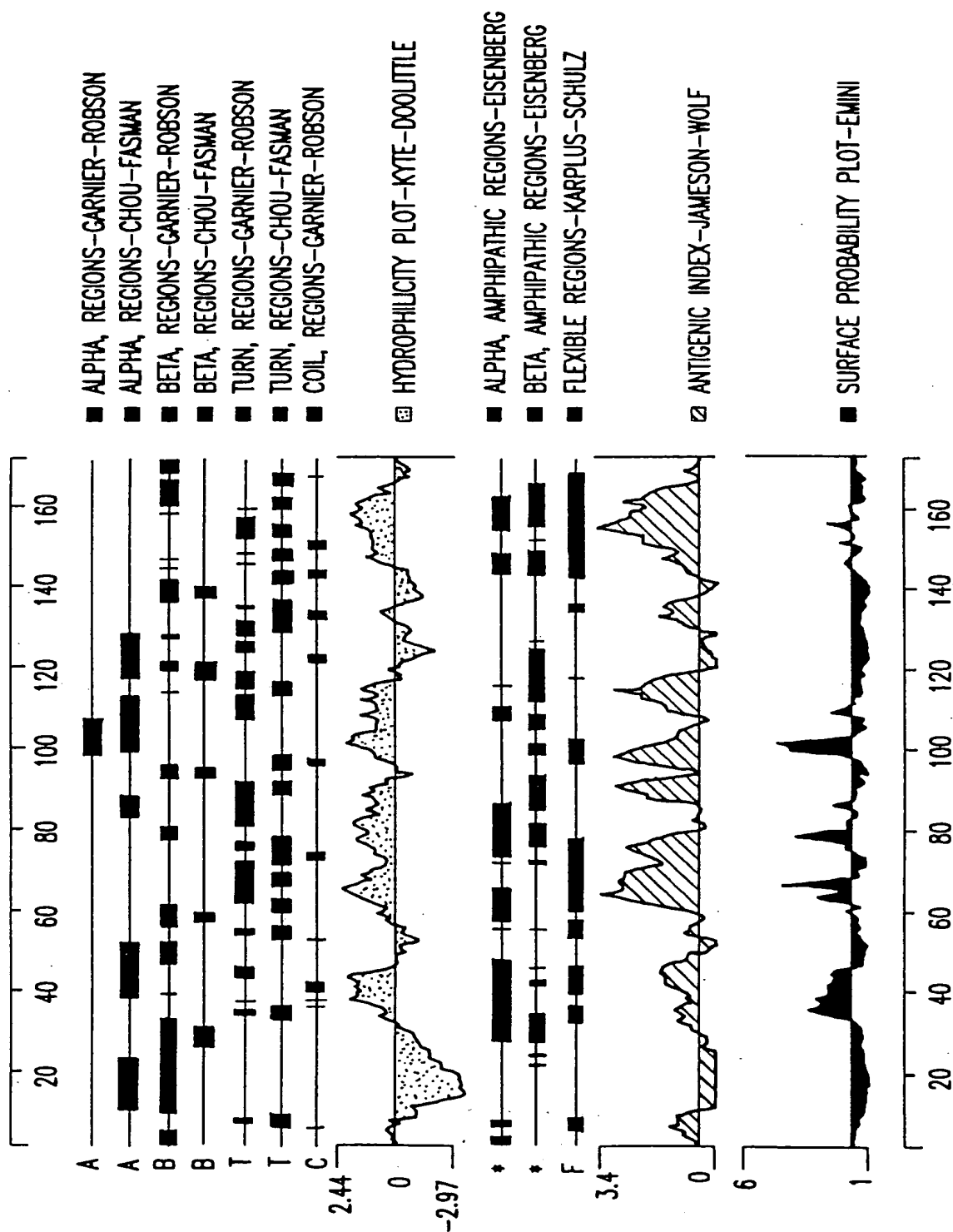


FIG.5

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HELDI06R

GGCACGAGCA GGGTCCTGTN TCCGCCCTGA GCCGCGCTCT NCCTGCTCCA GCAAGGACCA
TGAGGGCGCT GGAGGGGCCA GGCCTGTGCG TGCTGTGCCT GGTGTTGGCG CTGCCTGCCC
TGCTGCCGGT GCCGGCTGTA CGCGGAGTGG CAGAAACACN NACNTACCCC TGGCGGGACG
NAGAGACAGG GGAGCGGCTG GTGTNTNCCC ANTGCCCCC AGGCACCTTT NTGCAGCGGC
CGTGCCGNCG AGACAGCCCC ACGACGTGTG GCCCGTNTCC ACCGCGCCAC TACACGCATT
CTGGA ACTAC CTGGAGCGCT GNCGTTACTN CAACGTCCTC TCGGGGGAGC GTNAGGAGGA
GGCACGGGTT TNCCACGNCA ACCACAACCG NGGNTTACCG TNGCCGNACC GGTTCCTTCG
NCGCAAGTTG GTTTTTNNTT TGGAGNAAGG ATTCGTGTIN CAATTNATTG ACGNAGTGAT
TNNCNCGGG AACTNAAA

HCEOW38R

CGCAACTGCA CGGCCCTGGG ACTGGCCCTC AATGTGCCAG GNTCTTCCTC CCATGACACC
CTGTGCACCA GCTGCACTGG CTTCCCCCTC AGCACCAGGG TACCANGAGC TGAGGAGTGT
GAGCNTGCCG TCATCGACTT TTTGGCTTTC CAGGACATCT CCATCAAGAG GCTGCAGCGG
CTGCTCANGC C

FIG.6

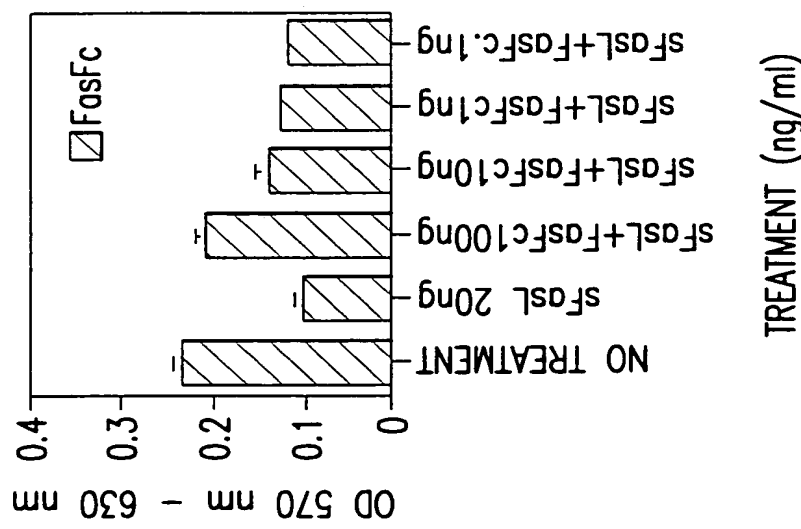


FIG. 7A

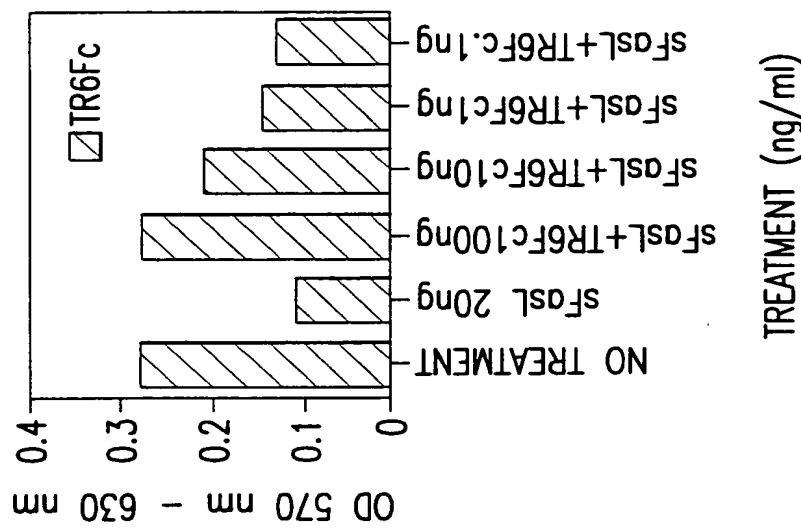


FIG. 7B